



Fig. 1

COesterase: domain 1 of 1, from 44 to 545; score 552.8, E = 2.3e-162

(SEQ ID NO:4)

Fbh53010FL	44	GWIQKQVTVLGSFVNVFLGVFFAAPLGSLRFTNPQ-ASPWDN	89
		vidatkypscldqddfgfslsdlkvalkmlslgwnklvglklSEDCLYL	
		+ At+yp+ ClQ++++ + + + + + g SEDCLYL	
Fbh53010FL	90	LRATSYPNLCLQNSEWLLDQH-----MLKVHPKFG--VSEDCLYL	130
		NVytPkntkpnsklpVnVwIhGGGFmGbsghslplslYdgesIaregnVI	
		N-y P+ + +sklpV+Vw +GG+F +Gs+ s dg++Ia+ ++V	
Fbh53010FL	131	NIYAPAHADTGSKLPVLVWFPGGAFKTGSA----SIFDGSALAAAYEDVL	175
		VVsiNYRLGplGLstgddklpssGNyGLLDQrLALKWVqdnIaaFGGDP	
		VV ++YRLG++GF++t d ++p GN++++DQ++AL WVq+NI FGGDP	
Fbh53010FL	176	VVVVQYRLGIFGFFTTWDQHAP--GNWAFKDQVAALSWSVQKNIEFFGGDP	223
		nVtIfGesAGaaSValllllsgGDNppskglFhRAIsqSGsaalspwai	
		+sVtIfGesaga SVs l+lS p++kgLFh+AI++SG a+ p	
Fbh53010FL	224	SSVTIFGESAGAISSVSLIS-----PMAKGLFHRAIMESGVAlIPYLE	267
		qseSnargrakelarilGcnetsssellcLrkskaeelLeatrSflfIe	
		++ + + +a + G n ++s++l+CLR k++elll ++++	
Fbh53010FL	268	AHDYKESDLQVVAHFCGNNASDSEALLRLRTKPSKELLTISQ--KTKS	315

Fig. 2A

Fbh53010FL	316	--FTR-----VVDGA-----FFPNEPLDLLSQAKFAIPSIIGVNNH	350
		YVPFLPLFIaGpVvDdDapeafipedeelikeGkfadvPylIGvtkd	
		f+ vVDG+ f+p +P++l+ ++ f+ +P +iGv+++	
		EGGyfaam.llnasskgedelkktndpvdvlellkyllyasealnkdM	
		E+G++++m+++++ +G ++ l++ l+ ++ + -	
Fbh53010FL	351	ECGFLLPmKEAPEILSG-----SNKSLALHLIQNILHIPPQ--	386
		ddladkvlekYpgdvdfsvesrkpnlgdmltDl1fKcptrivaadlhakh	
		++ v ++Y+ d + s + ++ l+d+l+D++F++p ++ ++ ++	
Fbh53010FL	387	--YLHLVANEYFHD-KH-SLTEIRDSLLDLGDVFFVVP-ALITARYHRD	431
		ggspVYaYvfdhpasfgigQflakrvdpfeggavHgdeIffvFgnpllke	
		+G+PvY+Y+f+h+++ +++p f++a+H+dE++fvFG +lk+	
Fbh53010FL	432	AGAPVYFYEFERHRPQC-----FEDTKPAFVKADHADDEVRFVFGGAFLKG	475
		qlyka...teeeeksskttmnywanFaktGnPnngtnglvvWpkytsee	
		+ +++++eek+++s+++mm+ywa+FA+tgNp ng 1 Wp+y+ +e	
Fbh53010FL	476	DIWMFegATEEEKLLSRKMMKYWATFARTGNP-NGN--DLSLWPAYNLTE	522
		qkvelllllttititaqklkardprkvlcnfw<*	
		q +l+ l + q+lK+ + ++fw	
Fbh53010FL	523	Q--YLQLDLNMSLGQRLKEPR-----VDFW	545

Fig. 2B